



## SEQUENCE LISTING

&lt;110&gt; Georgopoulos, Katia

<120> IKAROS REGULATORY ELEMENTS AND USES  
THEREOF

&lt;130&gt; 10287-067001

&lt;140&gt; US 09/755,830

&lt;141&gt; 2001-01-05

&lt;150&gt; US 08/283,300

&lt;151&gt; 1994-07-29

&lt;150&gt; US 08/238,212

&lt;151&gt; 1994-05-02

&lt;150&gt; US 08/121,438

&lt;151&gt; 1993-09-14

&lt;150&gt; US 07/946,233

&lt;151&gt; 1992-09-14

&lt;160&gt; 43

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1788

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (223)... (1515)

&lt;223&gt; mIk-2

&lt;400&gt; 1

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gaagaggaag aggaagagga atctgcggct catccaggga tcagggtcct tcccaagtgg 120  
ccactcagag gggactcaga gcaagtctag atttgtgtgg cagagagaga cagctctcgt 180  
ttggccttgg ggaggcacia gtctgttgat aacctgaaga ca atg gat gtc gat 234  
Met Asp Val Asp  
1

gag ggt caa gac atg tcc caa gtt tca gga aag gag agc ccc cca gtc 282  
Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu Ser Pro Pro Val  
5 10 15 20

agt gac act cca gat gaa ggg gat gag ccc atg cct gtc cct gag gac 330  
Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro Val Pro Glu Asp  
25 30 35

ctg tcc act acc tct gga gca cag cag aac tcc aag agt gat cga ggc 378  
Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys Ser Asp Arg Gly

a13

FASTSEQ "GENES" 4.0

40							45					50					
atg	ggt	gaa	cgg	cct	ttc	cag	tgc	aac	cag	tct	ggg	gcc	tcc	ttt	acc	426	
Met	Gly	Glu	Arg	Pro	Phe	Gln	Cys	Asn	Gln	Ser	Gly	Ala	Ser	Phe	Thr		
55			60					65									
cag	aaa	ggc	aac	ctc	ctg	cgg	cac	atc	aag	ctg	cac	tcg	ggt	gag	aag	474	
Gln	Lys	Gly	Asn	Leu	Leu	Arg	His	Ile	Lys	Leu	His	Ser	Gly	Glu	Lys		
70			75					80									
ccc	ttc	aaa	tgc	cat	ctt	tgc	aac	tat	gcc	tgc	cgc	cgg	agg	gac	gcc	522	
Pro	Phe	Lys	Cys	His	Leu	Cys	Asn	Tyr	Ala	Cys	Arg	Arg	Arg	Asp	Ala		
85		90					95			100							
ctc	acc	ggc	cac	ctg	agg	acg	cac	tcc	gtt	ggt	aag	cct	cac	aaa	tgt	570	
Leu	Thr	Gly	His	Leu	Arg	Thr	His	Ser	Val	Gly	Lys	Pro	His	Lys	Cys		
105				110					115								
gga	tat	tgt	ggc	cgg	agc	tat	aaa	cag	cga	agc	tct	tta	gag	gag	cat	618	
Gly	Tyr	Cys	Gly	Arg	Ser	Tyr	Lys	Gln	Arg	Ser	Ser	Leu	Glu	Glu	His		
120			125					130									
aaa	gag	cga	tgc	cac	aac	tac	ttg	gaa	agc	atg	ggc	ctt	ccg	ggc	gtg	666	
Lys	Glu	Arg	Cys	His	Asn	Tyr	Leu	Glu	Ser	Met	Gly	Leu	Pro	Gly	Val		
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tgc	cca	gtc	att	aag	gaa	gaa	act	aac	cac	aac	gag	atg	gca	gaa	gac	714	
Cys	Pro	Val	Ile	Lys	Glu	Glu	Thr	Asn	His	Asn	Glu	Met	Ala	Glu	Asp		
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ctg	tgc	aag	ata	gga	gca	gag	agg	tcc	ctt	gtc	ctg	gac	agg	ctg	gca	762	
Leu	Cys	Lys	Ile	Gly	Ala	Glu	Arg	Ser	Leu	Val	Leu	Asp	Arg	Leu	Ala		
165		170					175			180							
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Ser	Asn	Val	Ala	Lys	Arg	Lys	Ser	Ser	Met	Pro	Gln	Lys	Phe	Leu	Gly		
185				190					195								
gac	aag	tgc	ctg	tca	gac	atg	ccc	tat	gac	agt	gcc	aac	tat	gag	aag	858	
Asp	Lys	Cys	Leu	Ser	Asp	Met	Pro	Tyr	Asp	Ser	Ala	Asn	Tyr	Glu	Lys		
200			205					210									
gag	gat	atg	atg	aca	tcc	cac	gtg	atg	gac	cag	gcc	atc	aac	aat	gcc	906	
Glu	Asp	Met	Met	Thr	Ser	His	Val	Met	Asp	Gln	Ala	Ile	Asn	Asn	Ala		
215			220					225									
atc	aac	tac	ctg	ggg	gct	gag	tcc	ctg	cgc	cca	ttg	gtg	cag	aca	ccc	954	
Ile	Asn	Tyr	Leu	Gly	Ala	Glu	Ser	Leu	Arg	Pro	Leu	Val	Gln	Thr	Pro		
230			235					240									
ccc	ggt	agc	tcc	gag	gtg	gtg	cca	gtc	atc	agc	tcc	atg	tac	cag	ctg	1002	
Pro	Gly	Ser	Ser	Glu	Val	Val	Pro	Val	Ile	Ser	Ser	Met	Tyr	Gln	Leu		
245		250					255			260							
cac	aag	ccc	ccc	tca	gat	ggc	ccc	cca	cgg	tcc	aac	cat	tca	gca	cag	1050	
His	Lys	Pro	Pro	Ser	Asp	Gly	Pro	Pro	Arg	Ser	Asn	His	Ser	Ala	Gln		
265				270					275								

1. The first step is to identify the problem. This involves understanding the current situation and what needs to be improved.

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<210> 2
<211> 1386
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1386)
<223> hIk-1
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a.3

# THE UNIVERSITY OF CHICAGO

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 Gln Lys Phe Leu Gly Asp Lys Gly Leu Ser Asp Thr Pro Tyr Asp Ser  
 225 230 235 240

gcc acg tac gag aag gag aac gaa atg atg aag tcc cac gtg atg gac 768  
 Ala Thr Tyr Glu Lys Glu Asn Glu Met Met Lys Ser His Val Met Asp  
 245 250 255

caa gcc atc aac aac gcc atc aac tac ctg ggg gcc gag tcc ctg cgc 816  
 Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg  
 260 265 270

ccg ctg gtg cag acg ccc ccg ggc ggt tcc gag gtg gtc ccg gtc atc 864  
 Pro Leu Val Gln Thr Pro Pro Gly Gly Ser Glu Val Val Pro Val Ile  
 275 280 285

agc ccg atg tac cag ctg cac agg cgc tcc gag ggc acc ccg cgc tcc 912  
 Ser Pro Met Tyr Gln Leu His Arg Arg Ser Glu Gly Thr Pro Arg Ser  
 290 295 300

aac cac tcc gcc cag gac agc gcc gtg gag tac ctg ctg ctg ctc tcc 960  
 Asn His Ser Ala Gln Asp Ser Ala Val Glu Tyr Leu Leu Leu Leu Ser  
 305 310 315 320

aag gcc aag ttg gtg ccc tcc gag cgc gag gcg tcc ccg agc aac agc 1008  
 Lys Ala Lys Leu Val Pro Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser  
 325 330 335

tgc caa gac tcc acg gac acc gag agc aac aac gag gag cag cgc agc 1056  
 Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Asn Glu Glu Gln Arg Ser  
 340 345 350

ggt ctt atc tac ctg acc aac cac atc gcc cga cgc gcg caa cgc gtg 1104  
 Gly Leu Ile Tyr Leu Thr Asn His Ile Ala Arg Arg Ala Gln Arg Val  
 355 360 365

tcc ctc aag gag gag cac cgc gcc tac gac ctg ctg cgc gcc gcc tcc 1152  
 Ser Leu Lys Glu Glu His Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser  
 370 375 380

gag aac tcc cag gac gcg ctc cgc gtg gtc agc acc agc ggg gag cag 1200  
 Glu Asn Ser Gln Asp Ala Leu Arg Val Val Ser Thr Ser Gly Glu Gln  
 385 390 395 400

atg aag gtg tac aag tgc gaa cac tgc cgg gtg ctc ttc ctg gat cac 1248  
 Met Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His  
 405 410 415

gtc atg tac acc atc cac atg ggc tgc cac ggc ttc cgt gat cct ttt 1296  
 Val Met Tyr Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe  
 420 425 430

gag tgc aac atg tgc ggc tac cac agc cag gac cgg tac gag ttc tcc 1344  
 Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser  
 435 440 445

tcc cac ata acg cga ggg gag cac cgc ttc cac atg agc taa 1386

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 3'-GGG-5'

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 450 455 460

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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (1) ... (1296)  
 <223> mIk-3

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 agc ccc cca gtc agt gac act cca gat gaa ggg gat gag ccc atg cct 96  
 Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro  
 20 25 30  
 gtc cct gag gac ctg tcc act acc tct gga gca cag cag aac tcc aag 144  
 Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys  
 35 40 45  
 agt gat cga ggc atg gcc agt aat gtt aaa gta gag act cag agt gat 192  
 Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp  
 50 55 60  
 gaa gag aat ggg cgt gcc tgt gaa atg aat ggg gaa gaa tgt gca gag 240  
 Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu  
 65 70 75 80  
 gat tta cga atg ctt gat gcc tcg gga gag aaa atg aat ggc tcc cac 288  
 Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His  
 85 90 95  
 agg gac caa ggc agc tcg gct ttg tca gga gtt gga ggc att cga ctt 336  
 Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu  
 100 105 110  
 cct aac gga aaa cta aag tgt gat atc tgt ggg atc gtt tgc atc ggg 384  
 Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly  
 115 120 125  
 ccc aat gtg ctc atg gtt cac aaa aga agt cat act ggt gaa cgg cct 432  
 Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro  
 130 135 140  
 ttc cag tgc aac cag tct ggg gcc tcc ttt acc cag aaa ggc aac ctc 480  
 Phe Gln Cys Asn Gln Ser Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu  
 145 150 155 160  
 ctg cgg cac atc aag ctg cac tcg ggt gag aag ccc ttc aaa tgc cat 528  
 Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys His

	165	170	175	
ctt tgc aac tat gcc tgc cgc cgg agg gac gcc ctc acc ggc cac ctg				576
Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu				
	180	185	190	
agg acg cac tcc gga gac aag tgc ctg tca gac atg ccc tat gac agt				624
Arg Thr His Ser Gly Asp Lys Cys Leu Ser Asp Met Pro Tyr Asp Ser				
	195	200	205	
gcc aac tat gag aag gag gat atg atg aca tcc cac gtg atg gac cag				672
Ala Asn Tyr Glu Lys Glu Asp Met Met Thr Ser His Val Met Asp Gln				
	210	215	220	
gcc atc aac aat gcc atc aac tac ctg ggg gct gag tcc ctg cgc cca				720
Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg Pro				
	225	230	235	240
ttg gtg cag aca ccc ccc ggt agc tcc gag gtg gtg cca gtc atc agc				768
Leu Val Gln Thr Pro Pro Gly Ser Ser Glu Val Val Pro Val Ile Ser				
	245	250	255	
tcc atg tac cag ctg cac aag ccc ccc tca gat ggc ccc cca cgg tcc				816
Ser Met Tyr Gln Leu His Lys Pro Pro Ser Asp Gly Pro Pro Arg Ser				
	260	265	270	
aac cat tca gca cag gac gcc gtg gat aac ttg ctg ctg ctg tcc aag				864
Asn His Ser Ala Gln Asp Ala Val Asp Asn Leu Leu Leu Leu Ser Lys				
	275	280	285	
gcc aag tct gtg tca tgc gag cga gag gcc tcc ccg agc aac agc tgc				912
Ala Lys Ser Val Ser Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys				
	290	295	300	
caa gac tcc aca gat aca gag agc aac gcg gag gaa cag cgc agc ggc				960
Gln Asp Ser Thr Asp Thr Glu Ser Asn Ala Glu Glu Gln Arg Ser Gly				
	305	310	315	320
ctt atc tac cta acc aac cac atc aac ccg cat gca cgc aat ggg ctg				1008
Leu Ile Tyr Leu Thr Asn His Ile Asn Pro His Ala Arg Asn Gly Leu				
	325	330	335	
gct ctc aag gag gag cag cgc gcc tac gag gtg ctg agg gcg gcc tca				1056
Ala Leu Lys Glu Glu Gln Arg Ala Tyr Glu Val Leu Arg Ala Ala Ser				
	340	345	350	
gag aac tgc cag gat gcc ttc cgt gtg gtc agc acg agt ggc gag cag				1104
Glu Asn Ser Gln Asp Ala Phe Arg Val Val Ser Thr Ser Gly Glu Gln				
	355	360	365	
ctg aag gtg tac aag tgc gaa cac tgc cgc gtg ctc ttc ctg gat cac				1152
Leu Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His				
	370	375	380	
gtc atg tat acc att cac atg ggc tgc cat ggc tgc cat ggc ttt cgg				1200
Val Met Tyr Thr Ile His Met Gly Cys His Gly Cys His Gly Phe Arg				
	385	390	395	400

165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

cta aag tgt gat atc tgt ggg atc gtt tgc atc ggg ccc aat gtg ctc 618



Leu	Lys	Cys	Asp	Ile	Cys	Gly	Ile	Val	Cys	Ile	Gly	Pro	Asn	Val	Leu	
			120					125					130			
atg	gtt	cac	aaa	aga	agt	cat	act	ggg	gaa	cgg	cct	ttc	cag	tgc	aac	666
Met	Val	His	Lys	Arg	Ser	His	Thr	Gly	Glu	Arg	Pro	Phe	Gln	Cys	Asn	
			135				140					145				
cag	tct	ggg	gcc	tcc	ttt	acc	cag	aaa	ggc	aac	ctc	ctg	cgg	cac	atc	714
Gln	Ser	Gly	Ala	Ser	Phe	Thr	Gln	Lys	Gly	Asn	Leu	Leu	Arg	His	Ile	
			150			155					160					
aag	ctg	cac	tcg	ggg	gag	aag	ccc	ttc	aaa	tgc	cat	ctt	tgc	aac	tat	762
Lys	Leu	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	His	Leu	Cys	Asn	Tyr	
					170					175					180	
gcc	tgc	cgc	cgg	agg	gac	gcc	ctc	acc	ggc	cac	ctg	agg	acg	cac	tcc	810
Ala	Cys	Arg	Arg	Arg	Asp	Ala	Leu	Thr	Gly	His	Leu	Arg	Thr	His	Ser	
				185					190					195		
gtt	ggg	aag	cct	cac	aaa	tgt	gga	tat	tgt	ggc	cgg	agc	tat	aaa	cag	858
Val	Gly	Lys	Pro	His	Lys	Cys	Gly	Tyr	Cys	Gly	Arg	Ser	Tyr	Lys	Gln	
			200					205					210			
cga	agc	tct	tta	gag	gag	cat	aaa	gag	cga	tgc	cac	aac	tac	ttg	gaa	906
Arg	Ser	Ser	Leu	Glu	Glu	His	Lys	Glu	Arg	Cys	His	Asn	Tyr	Leu	Glu	
			215				220					225				
agc	atg	ggc	ctt	ccg	ggc	gtg	tgc	cca	gtc	att	aag	gaa	gaa	act	aac	954
Ser	Met	Gly	Leu	Pro	Gly	Val	Cys	Pro	Val	Ile	Lys	Glu	Glu	Thr	Asn	
			230			235						240				
cac	aac	gag	atg	gca	gaa	gac	ctg	tgc	aag	ata	gga	gca	gag	agg	tcc	1002
His	Asn	Glu	Met	Ala	Glu	Asp	Leu	Cys	Lys	Ile	Gly	Ala	Glu	Arg	Ser	
			245			250				255					260	
ctt	gtc	ctg	gac	agg	ctg	gca	agc	aat	gtc	gcc	aaa	cgt	aag	agc	tct	1050
Leu	Val	Leu	Asp	Arg	Leu	Ala	Ser	Asn	Val	Ala	Lys	Arg	Lys	Ser	Ser	
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atg	cct	cag	aaa	ttt	ctt	gga	gac	aag	tgc	ctg	tca	gac	atg	ccc	tat	1098
Met	Pro	Gln	Lys	Phe	Leu	Gly	Asp	Lys	Cys	Leu	Ser	Asp	Met	Pro	Tyr	
			280					285					290			
gac	agt	gcc	aac	tat	gag	aag	gag	gat	atg	atg	aca	tcc	cac	gtg	atg	1146
Asp	Ser	Ala	Asn	Tyr	Glu	Lys	Glu	Asp	Met	Met	Thr	Ser	His	Val	Met	
			295				300					305				
gac	cag	gcc	atc	aac	aat	gcc	atc	aac	tac	ctg	ggg	gct	gag	tcc	ctg	1194
Asp	Gln	Ala	Ile	Asn	Asn	Ala	Ile	Asn	Tyr	Leu	Gly	Ala	Glu	Ser	Leu	
			310			315					320					
cgc	cca	ttg	gtg	cag	aca	ccc	ccc	ggg	agc	tcc	gag	gtg	gtg	cca	gtc	1242
Arg	Pro	Leu	Val	Gln	Thr	Pro	Pro	Gly	Ser	Ser	Glu	Val	Val	Pro	Val	
					330					335					340	
atc	agc	tcc	atg	tac	cag	ctg	cac	aag	ccc	ccc	tca	gat	ggc	ccc	cca	1290
Ile	Ser	Ser	Met	Tyr	Gln	Leu	His	Lys	Pro	Pro	Ser	Asp	Gly	Pro	Pro	

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Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys  
35 40 45

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 Ser Asp Arg Gly Met Gly Glu Arg Pro Phe Gln Cys Asn Gln Ser Gly  
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Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His  
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Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg  
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cgg agg gac gcc ctc acc ggc cac ctg agg acg cac tcc gtc att aag 336  
Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Ile Lys  
100 105 110

gaa gaa act aac cac aac gag atg gca gaa gac ctg tgc aag ata gga 384  
Glu Glu Thr Asn His Asn Glu Met Ala Glu Asp Leu Cys Lys Ile Gly  
115 120 125

gca gag agg tcc ctt gtc ctg gac agg ctg gca agc aat gtc gcc aaa 432  
Ala Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala Lys  
130 135 140

cgt aag agc tct atg cct cag aaa ttt ctt gga gac aag tgc ctg tca 480  
Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Cys Leu Ser  
145 150 155 160

gac atg ccc tat gac agt gcc aac tat gag aag gag gat atg atg aca 528  
Asp Met Pro Tyr Asp Ser Ala Asn Tyr Glu Lys Glu Asp Met Met Thr  
165 170 175

tcc cac gtg atg gac cag gcc atc aac aat gcc atc aac tac ctg ggg 576  
Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly  
180 185 190

gct gag tcc ctg cgc cca ttg gtg cag aca ccc ccc ggt agc tcc gag 624  
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 Asp Gly Pro Pro Arg Ser Asn His Ser Ala Gln Asp Ala Val Asp Asn  
 225 230 235 240

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 245 250 255

tcc ccg agc aac agc tgc caa gac tcc aca gat aca gag agc aac gcg 816  
 Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Ala  
 260 265 270

gag gaa cag cgc agc ggc ctt atc tac cta acc aac cac atc aac ccg 864  
 Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn His Ile Asn Pro  
 275 280 285

cat gca cgc aat ggg ctg gct ctc aag gag gag cag cgc gcc tac gag 912  
 His Ala Arg Asn Gly Leu Ala Leu Lys Glu Glu Gln Arg Ala Tyr Glu  
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 Val Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala Phe Arg Val Val  
 305 310 315 320

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 Ser Thr Ser Gly Glu Gln Leu Lys Val Tyr Lys Cys Glu His Cys Arg  
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 Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His  
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 Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly Tyr  
 355 360 365

cac agc cag gac agg tac gag ttc tca tcc cat atc acg cgg ggg gag 1152  
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agc ccc cca gtc agt gac act cca gat gaa ggg gat gag ccc atg cct	96
Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro	
20 25 30	
gtc cct gag gac ctg tcc act acc tct gga gca cag cag aac tcc aag	144
Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys	
35 40 45	
agt gat cga ggc atg gcc agt aat gtt aaa gta gag act cag agt gat	192
Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp	
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gaa gag aat ggg cgt gcc tgt gaa atg aat ggg gaa gaa tgt gca gag	240
Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu	
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gat tta cga atg ctt gat gcc tcg gga gag aaa atg aat ggc tcc cac	288
Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His	
85 90 95	
agg gac caa ggc agc tcg gct ttg tca gga gtt gga ggc att cga ctt	336
Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu	
100 105 110	
cct aac gga aaa cta aag tgt gat atc tgt ggg atc gtt tgc atc ggg	384
Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly	
115 120 125	
ccc aat gtg ctc atg gtt cac aaa aga agt cat act gga gac aag tgc	432
Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Asp Lys Cys	
130 135 140	
ctg tca gac atg ccc tat gac agt gcc aac tat gag aag gag gat atg	480
Leu Ser Asp Met Pro Tyr Asp Ser Ala Asn Tyr Glu Lys Glu Asp Met	
145 150 155 160	
atg aca tcc cac gtg atg gac cag gcc atc aac aat gcc atc aac tac	528
Met Thr Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr	
165 170 175	
ctg ggg gct gag tcc ctg cgc cca ttg gtg cag aca ccc ccc ggt agc	576
Leu Gly Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly Ser	
180 185 190	
tcc gag gtg gtg cca gtc atc agc tcc atg tac cag ctg cac aag ccc	624
Ser Glu Val Val Pro Val Ile Ser Ser Met Tyr Gln Leu His Lys Pro	
195 200 205	
ccc tca gat ggc ccc cca cgg tcc aac cat tca gca cag gac gcc gtg	672
Pro Ser Asp Gly Pro Pro Arg Ser Asn His Ser Ala Gln Asp Ala Val	

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gat aac ttg ctg ctg ctg tcc aag gcc aag tct gtg tca tcg gag cga			720
Asp Asn Leu Leu Leu Leu Ser Lys Ala Lys Ser Val Ser Ser Glu Arg			
225	230	235	240
gag gcc tcc ccg agc aac agc tgc caa gac tcc aca gat aca gag agc			768
Glu Ala Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser			
	245	250	255
aac gcg gag gaa cag cgc agc ggc ctt atc tac cta acc aac cac atc			816
Asn Ala Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn His Ile			
	260	265	270
aac ccg cat gca cgc aat ggg ctg gct ctc aag gag gag cag cgc gcc			864
Asn Pro His Ala Arg Asn Gly Leu Ala Leu Lys Glu Glu Gln Arg Ala			
	275	280	285
tac gag gtg ctg agg gcg gcc tca gag aac tcg cag gat gcc ttc cgt			912
Tyr Glu Val Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala Phe Arg			
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gtg gtc agc acg agt ggc gag cag ctg aag gtg tac aag tgc gaa cac			960
Val Val Ser Thr Ser Gly Glu Gln Leu Lys Val Tyr Lys Cys Glu His			
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tgc cgc gtg ctc ttc ctg gat cac gtc atg tat acc att cac atg ggc			1008
Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly			
	325	330	335
tgc cat ggc tgc cat ggc ttt cgg gat ccc ttt gag tgt aac atg tgt			1056
Cys His Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys			
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Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg			
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act Thr	ggc Gly 50	cac His	ctg Leu	agg Arg	acg Thr	cac His 55	tcc Ser	gtc Val	att Ile	aaa Lys	gaa Glu 60	gaa Glu	act Thr	aag Lys	cac His	192
agt Ser 65	gaa Glu	atg Met	gca Ala	gaa Glu	gac Asp 70	ctg Leu	tgc Cys	aag Lys	ata Ile	gga Gly 75	tca Ser	gag Glu	aga Arg	tct Ser	ctc Leu 80	240
gtg Val	ctg Leu	gac Asp	aga Arg 85	cta Leu	gca Ala	agt Ser	aat Asn	gtc Val 90	gcc Ala	aaa Lys	cgt Arg	aag Lys	agc Ser	tct Ser 95	atg Met	288
cct Pro	cag Gln	aaa Lys	ttt Phe 100	ctt Leu	ggg Gly	gac Asp	aag Lys	ggc Gly 105	ctg Leu	tcc Ser	gac Asp	acg Thr	ccc Pro 110	tac Tyr	gac Asp	336
agt Ser	gcc Ala	acg Thr 115	tac Tyr	gag Glu	aag Lys	gag Glu	aac Asn 120	gaa Glu	atg Met	atg Met	aag Lys	tcc Ser 125	cac His	gtg Val	atg Met	384
gac Asp 130	caa Gln	gcc Ala	atc Ile	aac Asn	aac Asn	gcc Ala 135	atc Ile	aac Asn	tac Tyr	ctg Leu	ggg Gly 140	gcc Ala	gag Glu	tcc Ser	ctg Leu	432
cgc Arg 145	ccg Pro	ctg Leu	gtg Val	cag Gln	acg Thr	ccc Pro	ccg Pro	ggc Gly	ggt Gly	tcc Ser	gag Glu	gtg Val	gtc Val	ccg Pro	gtc Val 160	480
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tcc Ser	aag Lys	gcc Ala 195	aag Lys	ttg Leu	gtg Val	ccc Pro	tcg Ser	gag Glu 200	cgc Arg	gag Glu	gcg Ala	tcc Ser 205	ccg Pro	agc Ser	aac Asn	624
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Gln	Met	Lys	Val	Tyr	Lys	Cys	Glu	His	Cys	Arg	Val	Leu	Phe	Leu	Asp		
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Phe	Glu	Cys	Asn	Met	Cys	Gly	Tyr	His	Ser	Gln	Asp	Arg	Tyr	Glu	Phe		
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Lys	Leu	Lys	Cys	Asp	Ile	Cys	Gly	Ile	Xaa	Cys	Ile	Gly	Pro	Asn	Val	
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Asn	Gln	Cys	Gly	Ala	Ser	Phe	Thr	Gln	Lys	Gly	Asn	Leu	Leu	Arg	His	
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Ile	Lys	Leu	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	His	Leu	Cys	Asn	
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Tyr	Ala	Cys	Arg	Arg	Arg	Asp	Ala	Leu	Thr	Gly	His	Leu	Arg	Thr	His	
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1. **Introduction**  
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 3. **Method**  
 4. **Results**  
 5. **Conclusion**  
 6. **References**  
 7. **Appendix**  
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**RESEARCH DESIGN**

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**Abstract** The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Ankara, Turkey. The study group consisted of 20 children (10 boys and 10 girls) who were randomly selected from the school. The children were divided into two groups: a control group and an experimental group. The control group did not participate in any physical education program, while the experimental group participated in a 12-week training program. The physical fitness of the children was measured at the beginning and at the end of the 12-week period. The measurements included heart rate, blood pressure, and body mass index. The results of the study showed that the experimental group had significantly higher heart rates and blood pressures at the end of the 12-week period compared to the control group. Additionally, the experimental group had a significantly lower body mass index at the end of the 12-week period compared to the control group. These findings suggest that a 12-week training program can improve the physical fitness of 10-year-old children.

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**THE UNIVERSITY OF CHICAGO**

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